

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 07:03:49 ; Search time 52.04 Seconds
(without alignments)
1275.521 Million cell updates/sec

Title: US-09-652-292-2
Perfect score: 2765
Sequence: 1 MCHSPVLPCLCASVSLGLG.....GHRQNSTGIPYSRIEISAAS 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2765	100.0	541	4	095528
2	932	33.7	621	6	09BE72
3	626.5	22.7	457	2	P96742
4	594.5	21.5	580	10	09C757
5	575	20.8	558	10	09F1F2
6	569.5	20.6	502	10	09FRP7
7	567	20.5	521	10	022848
8	545	19.7	580	10	09ZQP6
9	541	19.6	582	10	023492
10	529	19.1	574	10	09AUM9
11	529	19.1	581	10	09LKH2
12	526.5	19.0	581	10	09LKH1
13	521.5	18.9	433	2	09CFH3
14	519	18.8	534	10	09LLE1
15	516	18.7	470	10	09LLE0
16	515	18.6	555	10	09FXV8
17	508	18.4	493	10	023213
18	507	18.3	551	10	09LLE2
19	502	18.2	515	10	09LLE8

20	497	18.0	511	10	09XIH6
21	497	18.0	606	5	09XXR3
22	495.5	17.9	539	10	09LS92
23	495	17.9	560	10	09LFI3
24	491.5	17.8	542	10	09LLD9
25	491	17.8	473	2	005182
26	491	17.8	523	10	006312
27	488.5	17.7	464	2	P96710
28	488.5	17.7	522	10	09SXB1
29	488	17.6	519	10	09ZS76
30	485.5	17.6	479	2	09FDM0
31	484.5	17.5	511	10	09XIH7
32	483	17.5	516	10	004078
33	482.5	17.5	513	10	09FOX3
34	482	17.4	508	10	065413
35	480.5	17.4	545	10	P93076
36	480.5	17.4	549	10	P93075
37	480	17.4	477	4	09NSC4
38	475	17.2	519	10	09Z863
39	474.5	17.2	478	11	09JJ21
40	472	17.1	479	11	09JMA6
41	471.5	17.1	510	10	065322
42	471.5	17.1	639	5	Q21455
43	470	17.0	470	2	09KJVI
44	470	17.0	477	4	09NY64
45	468	16.9	475	10	048537

ALIGNMENTS

RESULT 1

ID	095528	PRELIMINARY:	PRT:	541 AA.
AC	095528; 09H416;			
DC	01-MAY-1999 (TRENBLrel. 10, Created)			
DT	01-JUN-2001 (TRENBLrel. 17, Last sequence update)			
DE	01-JUN-2001 (TRENBLrel. 17, Last annotation update)			
DE	DJ28H20.1 (SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 10) (HYPOTHETICAL 56.9 KDA PROTEIN) (FACILITATIVE GLUCOSE TRANSPORTER GLUT10).			
GN	SLC2A10 OR GLUT10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ramsay.H.;			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Stavrides G.S., Hashim Y., Huckle E.J., Deloukas P.;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Fossey S.C., Mihic S.J., Craddock A.L., Mychalecky J.C., Dawson P.A., Bowden D.W.;			
RT	*GLUT10: A novel glucose transporter in the type 2 diabetes linked region of chromosome 20q12-13.1.*;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21145593; Pubmed=11247674;			
RA	McVie-Wylie A.J., Lamson D.R., Chen Y.T.;			
RT	*Molecular Cloning of a Novel Member of the GLUT Family of Transportsers, SLC2A10 (GLUT10), Localized on Chromosome 20q13.1: A Candidate Gene for NIDDM Susceptibility.*;			
RL	Genomics 72:113-117(2001).			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.			
DR	EMBL; AL031055; CAA19926.2; -.			
DR	EMBL; AL137188; CAB69822.2; -.			

09xib6 arabidopsis	
09xir3 caenorhabdi	
09is92 arabidopsis	
09lf13 arabidopsis	
09l1d9 zen mays (m	
005182 bacillus me	
006312 nicotiana t	
P96710 bacillus su	
09sxb1 arabidopsis	
09z876 vitis vinif	
09fcm0 zymomonas m	
004078 vicia faba	
09fqk3 apium grave	
065413 arabidopsis	
P93076 beta vulgar	
P93075 beta vulgar	
09nec4 homo sapien	
09zr63 vitis vinif	
09jj21 rattus norv	
09jma6 rattus norv	
065322 petunia hyb	
Q21455 caenorhabdi	
09kiv1 lactobacilli	
09ny64 homo sapien	
048537 prunus arme	

DR EMBL; AF248053; AAK31911.1; -
 DR EMBL; AF321240; AAK26294.1; -
 DR InterPro; IPR003662; sub.transporter.
 DR InterPro; IPR003663; Sugar_transporter.
 DR Pfam; PF00083; sugar_cr; 1.
 DR PRINTS; PR00171; SUGTRNSPORT.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN.1.
 KW Hypothetical protein; Sugar transport; Transmembrane.
 SQ SEQUENCE 541 AA; 56911 MW; 6D644525FAL36908 CRC64;

Query Match 100.0%; Score 2765; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.6e-152;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGHSPVPLPCASVSLGGLTGTYELAVISGALLPLQDPLGSLCEQEFVLSGLLIGALL 60
 DB 1 MGHSPVPLPCASVSLGGLTGTYELAVISGALLPLQDPLGSLCEQEFVLSGLLIGALL 60
 QY 61 ASLVGGFLIDCYGRKQAILGSLNVLVLAGSLTLGLAGSLAWLVGRAVVGFAISLSMACC 120
 DB 61 ASLVGGFLIDCYGRKQAILGSLNVLVLAGSLTLGLAGSLAWLVGRAVVGFAISLSMACC 120
 QY 121 IYVSELVGRQGVLSVLEAGTIVGILLSYALNYALAGTTPGWRHMFQWATAPAVLQSL 180
 DB 121 IYVSELVGRQGVLSVLEAGTIVGILLSYALNYALAGTTPGWRHMFQWATAPAVLQSL 180
 QY 181 SLFLPAGTDTATHKDLIPLQGGAPKLGPRPRYSFLDLFRANDMRGRTTVGLGLVL 240
 DB 181 SLFLPAGTDTATHKDLIPLQGGAPKLGPRPRYSFLDLFRANDMRGRTTVGLGLVL 240
 QY 241 FOOLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATITAMGLVDGRARRALL 300
 DB 241 FOOLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATITAMGLVDGRARRALL 300
 QY 301 LAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDGLLODSSLPIPTN 360
 DB 301 LAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDGLLODSSLPIPTN 360
 QY 361 EQOREPILSTAKTKPHRSGDPSAPPRALSSALPGPPLPARGHALLRWALLCLAVFV 420
 DB 361 EQOREPILSTAKTKPHRSGDPSAPPRALSSALPGPPLPARGHALLRWALLCLAVFV 420
 QY 421 SAFSFGFGVTVLWVLSVPEIRGAFARCNFNAANLFLISFLDLIGTIGLSWTF 480
 DB 421 SAFSFGFGVTVLWVLSVPEIRGAFARCNFNAANLFLISFLDLIGTIGLSWTF 480
 QY 481 LVGLFAVLGLGFIYLVFVPETKQSLAEIDQFQKRRTLSFGHRONSTGIPYSRIEISAA 540
 DB 481 LVGLFAVLGLGFIYLVFVPETKQSLAEIDQFQKRRTLSFGHRONSTGIPYSRIEISAA 540
 QY 541 S 541
 DB 541 S 541

RESULT 2
 Q9BE72 PRELIMINARY; PRT; 621 AA.
 AC Q9BE72
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 67.5 KDA PROTEIN
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL CORTEX;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RL libraries";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056798; BAB39322.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 621 AA; 67485 MW; 9E9384A2320AC716 CRC64;

Query Match 33.7%; Score 932; DB 6; Length 621;
 Best Local Similarity 39.2%; Pred. No. 1.8e-46;
 Matches 216; Conservative 85; Mismatches 178; Indels 72; Gaps 7;

QY 10 LCASVSLGGLTFGEYELAVISGALLPLQDPLGSLCEQEFVLSGLLIGALLASLVGGFLI 69
 DB 46 LSSVTAAGSLGVLGELGIISGALLQIKLLTSLSCHEQEMVVSLLIGALLASLVGGVLI 105
 QY 70 DCYGRKQATLGSNLVLAGSLTLGLAGSLAWLVGRAVVGFAISLSMACCIVVSELVGP 129
 DB 106 DRYGRTAILSSCILGLGSIVLILSLSTVLIVGRIAGVISLSLSIATCVYIAEAPQ 165
 QY 130 RQGVLSVLEAGTIVGILLSYALNYALAGTTPGWRHMFQWATAPAVLQSLFLPAGT 189
 DB 166 HRRGLVSLNLMIVIGILSAVISNVAEAFVHKYKMFGLVPLGILQAIAMVFLPSS- 224
 QY 190 DETATHKDIPLQGGAPKLGPRPR-----YSPFLDLFRARD 226
 DB 225 -----PFLVKNKGOGAASKV-LGRRLALSDATEELTVIKSSLKDEYOYSPWDLFRSKD 277
 QY 227 NMRGTTVGLGLVLPQQLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATLT 286
 DB 278 NMRTRIMIGLTVLPVQITGQPNILFYASTVLKSVGFOSNEAASLSTAGVGVKVIPTIP 337
 QY 287 AMGLVDGRARRALLLAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDGLLODSSLPIPTN 360
 DB 338 ATLLVDHVGSKTFLCIGSSVMAASLVMTGIVNLNTHMFTNCRSHNSINOSLDESIVG 397
 QY 327 PSCLAVPNATGOTGLPGDGLLODSSLPIPTN-----PIPTNEDQREPILSTAKTKPHRSGDP 383
 DB 398 PGNLSASNTURDFKGIASHRSLSMLPRNDVDKRGETTSSASLLNAVLSHTEYOIVTDP 457
 QY 394 SAPPRALSSALPGPPLPARGHALLRWALLCLAVFVSAFSGFGVTVLWVLSVPEI 443
 DB 458 GDVP-----AFLKWLASLLVYAAFSIGLGPMPWLVSSEIFPGI 499
 QY 444 RGRAFCNFMNAANLFLISFLDLIGTIGLSWTFLLYGLTAVLGLGFIYLVFVPETKQ 503
 DB 500 RGRAVLTSSMNGINLLISLTLFTVTDLIGLPMWCVFIYTIMSLASLLFVVMFIPETKGC 559
 QY 504 SLAEIDQFQK 514
 DB 560 SLEQISMELAK 570

RESULT 3
 P96742 PRELIMINARY; PRT; 457 AA.
 AC P96742
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE SIMILAR TO METABOLITE TRANSPORT PROTEINS.
 GN YWFG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Lelong C., Glaser P., Presecan E., Dauchin A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]


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Query Match          21.5%; Score 594.5; DB 10; Length 580;
Best Local Similarity 29.6%; Pred. No. 5.5e-27;
Matches 173; Conservative 94; Mismatches 217; Indels 101; Gaps 16;

QY 4 SPVPVLCASVSLGGTGFYELAVISGALLPIQLDF---GLSCLEOEFVLGSLLLGALL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 NPVYLRFAFSAG-IGGLFGYDGTGVSIGALLYIRDDFKSVDRNTWLQGVSMVAVCAIV 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 ASLVGGFLIDCYGRKQAILGSNLVLLAGSLTGLAGSLAWLVLGRVAVGFSAISMACC 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 84 GAALGGWANDKLGRSAILMADELFLUGAIIAAMPSSLVYGVGVFVLGVGMASMTAP 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 IYVSELVGPRQGVLYSEAGITVGLLSVALYNALAGTPWGRWHMFGNATPAVLQSL 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 LYISEASPAKIRGALYSTNGFLITGGQFLSYLINLATDVTGTRWMLGIAGIPALLOFV 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 SLILFLP-----AGTDETA-----THKDLIP---LQGGEAPKILGP 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 LMTFLPESRMLYRKGRHEEAKAILRRIYGAEDVEQIRALKDSVETEILLEGSSEKI-- 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 GRPRYSLDLFRANDNNRGRTTVGLGLVLFQOLTGPQNVLCYASTLFSVGVFHGSSAVL 271
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 -----NMIKCKAKTVRG-LIAGVGLQVQQFVGINTVMIYSPFTVOLAGFASNRITALL 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 272 ASVGLGAVKVAATLTAMGLVDAGRALLAGCALMSVSGICGLVSFAYPMDSGPSCLA 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 316 LSLVITAGLNAFGSIISYIFDIRGRKKLLI-----ISLFGV-IISLGI----- 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 332 VPNATG-----QTLGDCSL-----LQDSSLPIPTNEDQREPIILSTAKTKP----- 376
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 358 ---LTGVFYFAATHAPAISSLETQRNNISCPDYKKSAMTNWDCMTCLKASSPSGCGYCS 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 377 -----HPRS---GDPSAPP-----RLALSSALPGPPLPARGHALLRTALLCLMWFS 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 SPICKEHGACWISDDSVKDLCHNENRLWYTRGCP-----SNGFWFALLGLGLYII 465
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 AFSPGPGVTWLVELIYVEIICRPAFCNSFNWAAUNPISLFDLICTIGLSWTFL 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 466 FSPGGMGTVPWIVNSIYPLRFRCGCGGAATAANWISNLIVASOFLSLTAIGTSWTLI 525
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 YGTLAVLGLGFIYLFVPETKQGSLSAIDQOFQKRRTFLSGHRON 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 526 FGVISVIALFLVMVCPETKGMPEIEKMLERRSWEFPKWKKS 570
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
Q9FIF2 PRELIMINARY; PRT; 558 AA.
ID Q9FIF2 AC Q9FIF2
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SUGAR TRANSPORTER-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsidae.
NCBI_Taxid=3702;
{}
RN
RR
RP
RC STRAIN=COLUMBIA;
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5, VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:379-391(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BAB016890; BAB09770.1; -.
DR EMBL; AB016890; BAB09770.1; -.
DR InterPro; IPR003662; sub.transporter.
DR InterPro; IPR003663; Sugar_transporter.

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RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
RA Carreer A.J., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence.";
RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AC006068; AAD15441.1; -.
DR Medel; 39574; Arath; 3059; 39574.
DR InterPro; IPR003662; sub.transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 580 AA; 63171 MW; FC6437FD5A3E00B3 CRC64;

Query Match 19.7%; Score 545; DB 10; Length 580;
Best Local Similarity 28.6%; Pred. No. 4e-24;
Matches 164; Conservative 99; Mismatches 205; Indels 106; Gaps 18;

QY 4 SPVPLPCASVSLGGITFCGYELAVISGALLPLQLDFG----LSCLEDFVLVGLSLLGALL 60
DB 23 TPYIMRLALSAG-IGGLLFYNTGTAGALLYKEEFGEYDNTKLTQLEIIVTAVGAI 81

QY 61 ASLVGGFLIDCYGRKQAILGSLNVLGASLTGLAGSLAWLVGRAVGVFAISLSMACC 120
DB 82 GAATGGWYNDKFGRRMSVLADVLELLGLGAVVIAHPVVIILGLLVGVGVGMASMTSP 141

QY 121 IYVSELVGPQRGVLSVLEAGITVIGLLSYALNYALAGTTPGWRHMFGWATAPAVLQSL 180
DB 142 LYISESPARIRGALVSTNGLLITGGQFLSYLINLAFVHTPGTWKMLGVSALPAIIQFC 201

QY 181 SLFLPAG-----TDETATKDLI-----PLOGEA-----PKLGPRP 214
DB 202 LMLTLPESPRWLYRKDRKRAESRDILRIYPAEMVEAIAALKESVRAETADEIIG---- 257

QY 215 RYVFLDLFR-ARDN--MRGRTTVGLGLVLFQQLTGQPNVLCYASTIFSSVGRHGSSAV- 270
DB 258 -HTFSOKLRGALSNPVVRHGLAAGITVQVAQFVGINTVYVSPITLQFAGTASNKATAMA 316

QY 271 --LASVGLGAVKVAATLTAMGLVDVDRAGRRALLAGCALMALSVSGIGLVFAVPMDSGPS 328
DB 317 LALITSGLNAY--GSVSMFVDRYGRKLMT-----ISMFGII-----T 354

QY 329 CLAVPNATGQTGLPGDGLQDSSLPPIPTNEDQRE-----PILS--TAKTKPH-- 377
DB 355 CLVILAAVNEA-----SNHAPKIDK--RDSRFNAKNATCFAPADFTASR3PPSNW 403

QY 378 -----PRGDSAPRIALSSALPGPLPARGHALLR-----WTALLCL 416
DB 404 NCMKLCQYDCGFCNSGAQYAPAGACIVQSDMKALCHSKGRITFRDGCPSKFGYLAIVFL 463

QY 417 MYFVSASFSGFQVWLVLSLVEIYRIGRAPAFCSFNWAAFLPISFLDLITGLS 476
DB 464 GLYIIVAPGCMGTVPWVNSEIYPLRYRGLAGGIAAASNMNSNLVVSSETFLTITNAVGS 523

QY 477 WTFLLYGLTAVLGLGFIYLFVPETRGSLAEIDQ 510
DB 524 GFLLFAGSSAVGLFFIWLVPETRGQFEVEK 557

RESULT 9
O23492 ID O23492 PRELIMINARY; PRT; 582 AA.
AC O23492;
DT 01-JAN-1998 (TReMBRel. 05, Created)
DT 01-JAN-1998 (TReMBRel. 05, Last sequence update)
DT 01-JUN-2001 (TReMBRel. 17, Last annotation update)
DE SIMILARITY TO MEMBRANE TRANSPORT PROTEIN (MEMBRANE TRANSPORTER LIKE

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DE PROTEIN).
GN AT4G16480.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=98121113; PubMed=9461215;
RX Bevan M., Hancock I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terry N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., James R., Schaeffer M., Funk B., Muellner-Auer S.,
RA Silvey M., Pons A., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moore S., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Voickaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chaiwatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; 297341; CAB10424.1; -.
DR Medel; AL161544; CAB78690.1; -.
DR InterPro; IPR003662; sub.transporter.
DR InterPro; IPR003663; Sugar_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 582 AA; 62891 MW; FA8F8DDCA5D0CB0 CRC64;

Query Match 19.6%; Score 541; DB 10; Length 582;
Best Local Similarity 28.8%; Pred. No. 6.8e-24;
Matches 161; Conservative 91; Mismatches 231; Indels 76; Gaps 13;

QY 4 SPVPLPCASVSLGGITFCGYELAVISGALLPLQLDF---GLSCLEDFVLVGLSLLGALL 60
DB 24 TPYIMRLALSAG-IGGLLFYNTGTAGALLYKEEFGEYDNTKLTQLEIIVTAVGAI 82

QY 61 ASLVGGFLIDCYGRKQAILGSLNVLGASLTGLAGSLAWLVGRAVGVFAISLSMACC 120
DB 83 GAAVGGWINDKFGRRMSVLADVLELLGLGAVVIAHPVVIILGLLVGVGVGMASMTSP 142

QY 121 IYVSELVGPQRGVLSVLEAGITVIGLLSYALNYALAGTTPGWRHMFGWATAPAVLQSL 180
DB 143 LYISESPARIRGALVSTNGLLITGGQFLSYLINLAFVHTPGTWKMLGVSALPAIVQFV 202

QY 181 SLFLPAG-----TDETATKDLIPLQGEAPK-----LGPGR 213
DB 203 LMLSLPESPRWLYRKDRKRAESRAILERIYPADEVEAEALKL-SVEAKEADEAIIG--- 258

QY 214 PRYFLDLFRAR-----DNMRGRTTVGLGLVLFQQLTGQPNVLCYASTIFSSVGRHG 266
DB 259 -----DSFSAKLKGAFCNPPVVRGLAAGITVQVAQFVGINTVYVSPISVQFAGYASN 312

QY 267 SSAYLASVGLGAVKVAATLTAMGLVDVDRAGRRALL-----LAGCALMALSVSGIGLVSA 320
DB 313 KTAMALSITSGNALGSIVSMFVDRYGRKRLMIISFGLIACLIILATVFSQAAI-HA 371

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QY 321 VPMDSGPSCLAVPNATGOTGLPGDGLLQDSSLPPIPTNEDQREPIILSTAKKTKPHRPS 380
Db 372 PKIDAFESTTAPNATGAYAP-----LAAENAPP-----SRWCMKCLRSECGFCAS 419
QY 381 G-DPSAPPRALSSALPGPPLPARGHALLR-----WTALLCLMVFVSAPFSGFGPVT 431
Db 420 GVQYAPACACVVLSDDMKATCSSRRTFKDCPSKFGFLAIVLGLLIVVYAPGVTVP 479
QY 432 WLIVSEIYVPEIRGRAFAFCNFAANLFIISLFDLIGTIGLSWTLLYGLTAVLGLG- 491
Db 480 WIVNSEIYPLRYGLGGGTAASVNVSVNLIVSESLTHALGSGCTELLFAGPFTIGLF 539
QY 492 FYLFPVETKGSALAEIQ 510
Db 540 FIVLLVPETKGLQFBEVEK 558

RESULT 10
Q9AUM9 PRELIMINARY: PRT: 574 AA.
AC Q9AUM9:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE PUTATIVE SUGAR TRANSPORTER.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OX NCBI_TaxID=4530;
RN [1]
RA Spiegl L.A., King L., Kirchoff K.A., de la Bastide M., Preston R.R.,
RA Nascimento L.U., Vil M.D., Baker J.P., Miller B., Cunniss D.M.,
RA Kuit K.H., Rodriguez S., Santos L., Zutavern T., Ballja V.S.,
RA Shah R.S., Bahret A., Bal H.P., O'Shaughnessy A., Dedhia N.N.,
RA McCombie W.R.,
RA "Genomic Sequence for Oryza sativa, Nipponbare Strain, Chromosome X,
RT Clone OSJNB005B19, Complete Sequence."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC083945; AAK13147.1; -.
KW Sugar transport.
SQ SEQUENCE 574 AA; 60134 MW; 66042EF434ED05E6 CRC64;

Query Match 19.1%; Score 529; DB 10; Length 574;
Best Local Similarity 27.8%; Pred. No. 3.3e-23;
Matches 150; Conservative 83; Mismatches 192; Indels 114; Gaps 12;

QY 11 CASVSLGGLTGYELAVISGALLPLQDGLGSLCUEQELVGSLLGLLALLASLVGGLID 70
Db 86 CSIIGSIISVLNGYDTGVMSGAMLFKEDLKTNDTQOVVLGILNVCALVGSLSLAGRVS 145
QY 71 CVGRKQAILGSLNVLGAGSLTGLAGSLAVLGRVAVGFAISLSSMACCIIVSELVGR 130
Db 146 CVGRRLTSLAACIFLVGSVLMLAPNATLILAGRCVAGVGVGYALMIAPIYAAETASAD 205
QY 131 ORGVLSVLYEAGITVIGLLSYALNVALAGTP---WGRHMFHMGATAPVLQSLSLFLPAG 188
Db 206 IRGSLTSLPEICISGILIGYVANYLLAKPLVYGRWMLGALPLSAALAGVLAMPES 265
QY 189 -----TDETATHKDLIPLOG-----GEAPKLGPRPRYSFL 219
Db 266 PRLVVOGRAEALSVLRVCDRPEADARLAEIKAAAGLADDDGAAANAGSG-CKGVNR 324
QY 220 DLF-RARDNMGRRTTVGLVGLVLFQQLTGQPNVLCYASTIFSVGPHGSSAVLASVGLCA 278
Db 325 ELLHPTPPRRIVTAALGIHFOHLTGIEAVLYSPRIFRKAAGIASRNVLAATIGVGV 384
QY 279 VKVAATLTAMGLVDRAGRRALLLACCALMALSVSGIGLVSPAVPMDSGPSCLAVPNATCO 338
Db 385 TKTAELFALLLVDRIGRRPLVLS-----SLAGI-IASLA-----CLMG----- 423

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QY 339 TGLPGDGLLQDSSLPPIPTNEDQREPIILSTAKKTKPHRSGDPSAPPRALSSALPGP 398
Db 424 -----LTVIERSPPHHS----- 435
QY 399 PLPARGHALLRWTLALCL---MVFSAFSGFGPVTWLVLSLSEIYVPEIRGRAFAFCNFSN 455
Db 436 --PA-----NAVLAITATVTFVASFSIGVGPITWAYSSSEYVPLRLRAQASGVGVAIN 486
QY 456 WAANLFIISLFDLIGTIGLSWTLLYGLTAVLGLGFLYFVPETKGSALAEIQDQFQK 514
Db 487 RVMNAGVSMFTVSLYKAITIGCAFFLEAGLAVAAATFFYLLCPEQTQGRPLEEIEEVFSQ 545

RESULT 11
Q9LKH2 PRELIMINARY: PRT: 581 AA.
AC Q9LKH2:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PUTATIVE NA+/MYO-INOSITOL SYMPORTER.
GN ITR1.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RA Chauhan S., Forsthoefel N., Ran Y., Quigley F., Nelson D.E.,
RA Bohner H.J.,
RT "Na+/myo-inositol symporters and Na+/H+-antiporters in plant sodium
RT transport."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL: AF280431; AAF91431.1; -.
DR InterPro: IPR000566; Lipocin_cytFABP.
DR InterPro: IPR001991; Na_dicarboxyl_sypm.
DR InterPro: IPR003662; sub_transporter.
DR InterPro: IPR003663; Sugar_transporter.
DR Pfam: PF00083; sugar_tr_1.
DR PRINTS: PR00173; EDTRNSPORT.
DR PRINTS: PR00171; SUGTRNSPORT.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 581 AA; 62474 MW; EB7EBE1C36D46F1F CRC64;

Query Match 19.1%; Score 529; DB 10; Length 581;
Best Local Similarity 27.6%; Pred. No. 3.4e-23;
Matches 158; Conservative 98; Mismatches 225; Indels 92; Gaps 13;

QY 1 MGHSPVPVPLCASVSLGGLTGYELAVISGALLPLQDGLGSLCUEQELVGSLLGL 57
Db 21 VGTTEYINRLAEPASAG-IGLLFGYDTGVISGALLYIKEDFKVAQKTLQETIVAMAVAG 79
QY 58 ALLASLVGGLIDCYGRKQAILGSLNVLGAGSLTGLAGSLAVLGRVAVGFAISLSM 117
Db 80 AIVGAGLGGLNDKFKRKPMIVADILFUTGAIIMSVAPAPVWIIIGRIVVGLGVGMAS 139
QY 118 ACCIYVSELVGRQGRVLSVLYEAGITVIGLLSYALNVALAGTP---WGRHMFHMGATAPVL 177
Db 140 TAPLITSETSPAKIRGALCATNGLLTGCGQFVSYLVNLTGTRVKGTRWMLGVAAPAAI 199
QY 178 QSLSLFLPAG-----TDETATHKDLIPLOGEAPKLG 211
Db 200 OVVLMLTPESPRWLYRONKISEAEIILGRIYPPPOVKEEDSLKTSIENENADRKAUGE 259
QY 212 GRPRYSFLDLFPARDN---MRGRTTVGLVGLVLFQQLTGQPNVLCYASTIFSVVGVGGSSA 269

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Db 260 GN---AFVRAKRAWDNKVRRGLIAGISVLVAQOFVGINVTMYISPTIILQAGFASNSTA 316
QY 270 VLASVGLGAVKVAATITAMGLVDRAGRALLLA-----GCALMALSVS 312
Db 317 LALSIVTSGLVAGSIVSMFVDRGRRRLMIISMAFITCLVLSGLFYGAQAAPKIS 376
QY 313 GIGLVFAVPMDSGSPCLAVPNATG-----QTGL-PCDSGLLQDSSLPPIPTNEDQRE 365
Db 377 QLESSHFG-----ANSTCPAFASATSPDRWNCMTCLKASDCAFCSNSASEPHPCACVAQTS 432
QY 366 PILSTAKTKPHRPSGDPSPAPRLALSSALPGPLPARGHALLRWTTALLCLMVFVSASF 425
Db 433 TMNACLGK-----RIYTEGCP-----SKFGFMAIIVGLGIITYSF 471
QY 426 GFGPVTWLVSEIYVEIRGAPAFCSFN---WAANLFISSLFSLDLGLTGLSLWTELL 481
Db 472 GMGTVPWILNSEIYPLRYRG-----ICGGTAVTLKCANLIVSETFLTLALGSGTELL 527
QY 482 YGLTAVLGLGFIYLVFVPETKGSLAIEDQFOK 514
Db 528 YAGFSLIGLIVIFLLVPETKGLPIEDIERMLEK 560

RESULT 12
Q9LKH1 PRELIMINARY; PRT; 581 AA.
AC Q9LKH1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PUTATIVE Na+/MgO-INOSITOL SYMPORTER.
GN ITR2.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Chauhan S., Forsthoefel N., Ran Y., Quigley F., Nelson D.E.,
RA Bohnert H.J.;
RT "Na+/MgO-inositol symporters and Na+/H+-antiporters in plant sodium
RT transport."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AF280432; AAF91432.1;
DR InterPro; IPR000566; Lipocalin_cytfabp.
DR InterPro; IPR001991; Na_dicarboxyl_sym.
DR InterPro; IPR003662; sub_transporter.
DR InterPro; IPR003663; Sugar_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00173; EDTRNSPORT.
DR PRINTS; PR00171; SUGTRNSPORT.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 581 AA; 62818 MW; 5C8F9A150FBFA5FF CRC64;

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Query Match 19.0%; Score 526.5; DB 10; Length 581;
 Best Local Similarity 28.6%; Pred. No. 4.7e-23;
 Matches 164; Conservative 86; Mismatches 229; Indels 95; Gaps 12;

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QY 1 MCHSPVPLPCASVLLGLTFGYELAVISGALLPLQDF---GLSCLEQFVLGSLILG 57
Db 21 IGKPTIILRLAFSAG-IGGLFGYDTGVISGALLYIKEDFEVERKTKLQETIVAMAVAG 79
QY 58 ALLASLVGGLIDCVGRKQAILGNLVLGSLTLGLAGSLANLVLGRAVYGFALSLSSM 117
Db 80 ALIAGVGYLNDRGFRPALIIDLIFFIGATITSLAPWMLILGRITFVLGVLGNMAM 139
QY 118 ACCITVSELVGRGVLSVLYEAGITVIGILLSVALNYALAGTPWGRHRHMGFNATPAVL 177

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Db 140 TSPLYISESPTRISALVSTNGLLITGSQFLSYLINLGFTRVKGTWRMMLGVAAFPVF 199
QY 178 QSLSLFLPLPAG-----TDETATHKDLIPLQCGEAPKLP 211
Db 200 QLLMLSLPESPRWLYRKNKVVEAEAILARIYPPVEEEMRAKASIEYEMAEIGEIG 259
QY 212 GRPRYSFLDLFR---ARDNWRGRTTVGLGLVLPQOUTGQPNVLCYASTIFSSVGFHGGSS 268
Db 260 G-----SMLSKVRKAMGNKIVRRGLYAGITVOVAQFVGINTVMYISPTIQLAGFASNST 315
QY 269 AVLASVGLGAVKVAATLTAMGLVDRAGRALLAGCALNALSVSGIGLVSEFAVPMDSGSP 328
Db 316 ALALSIVTSGLVAGSIVSMFVDRGRRRLMI-----ISMFGII-----T 356
QY 329 CLAVPNATGOTGLPGDSGLLQDSSLPPIPTNEDQREPIILST--AKTKPHRPSGDPSPAP 386
Db 357 CLIVLAI-----GPFQAAAHAPKISHAESTHFGNLSTCPAYTTTRNPATWNCMT 406
QY 387 PRLAISSA-----LPG-----PPLPARGHALLRWTT-----ALLCLMVF 419
Db 407 LQAASECAECTNKGNQLLPGCVSRDTAMKVACHCKRYFTTEGCPKRGFLAVILLGAY 466
QY 420 VSAFSGFGPVTWLVSEIYVEIRGAPAFCSFNWAANLFISSLFSLDLGLTIGLSWTF 479
Db 467 IISYSPGMGTVPWIVNSEIYPLRYRGVGGIAAVSNWTSNLIVSETFLTLALGANGTF 526
QY 480 LLYGTVAVLGLGFIYLVFVPETKGSLAIEDQFOQ 513
Db 527 LLFAGFSAIGLVIFLLVPETKGLPIEEVEHMLE 560

RESULT 13
Q9CFH3 PRELIMINARY; PRT; 433 AA.
AC Q9CFH3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE D-XYLOSE PROTON-SYMPORTER.
GN XYL1.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ILL403;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis."
RL Genome Res. 0:0-0(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AE006381; AAK05601.1;
DR InterPro; IPR003662; sub_transporter.
DR InterPro; IPR003663; Sugar_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 433 AA; 46868 MW; A57BF50C4ABE70A0 CRC64;

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Query Match 18.9%; Score 521.5; DB 2; Length 433;
 Best Local Similarity 28.9%; Pred. No. 6.7e-23;
 Matches 146; Conservative 79; Mismatches 158; Indels 123; Gaps 11;

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QY 17 LGGLTFGYELAVISGALLPLQDFGLSCLEQ-----FLVGSLLIGALLASLV 64
Db 15 LGGLLFGYDTGVISGALL-----PIEKSNQVSSWAKWMEGNITAAVLKMGAVIGAV 65

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QY 65 GGFLIDCYGRKQAILGSLNVLGAGSLTGLAGSLAWLVLGRAVVGFAISLSSMACCIYVS 124
 Db 66 ICPMSDRFRKRLLSLVSFFVFGALGSLNSALIIISRVILGNVAGVSASALVPTYLS 125
 QY 125 ELVGPQRQGVLSVLEAGITVIGILLSYALNYALAGTPMGRHMFQWATAPAVLQSLSLIF 184
 Db 126 ELSPAKIRGVSTPMLMTGILLAYISYALKGVSGNHHMLGLATVPAALLFGLGLF 185
 QY 185 LPAGTDEATHKDLPLQGGREAPKLG-----PGRPRYSFLDL-FRARDNMGR----- 231
 Db 186 LPESPRFLVRHON-----EAGAREILGMINDPNSEAEISDQLMAKEKOGGLOELFQ 241
 QY 232 -----TTVGLGLVLFQOLTGPQNVLYCYASTIFSSVCFHGGSSAVLASVCLGAVKVAATLT 286
 Db 242 MBRPVLIMAIGLAIFQVWGCNTVLYFAPSIYVAVGF-GASAALLAHIGIGIFNVIVTVI 300
 QY 287 ANGLVDRAGRALLAGCALMALSVSGILVSFAVPMDSGSPCLAVPNATGOTGLPGDSG 346
 Db 301 AMRVMDKVNRRMLNFGAGM-----GISLVLMSVGM-----ILAENA----- 338
 QY 347 LLDSSLPPIPTNEDQREPILSTAKTKPHPRSGDPSAPPRLALSSALPGPPLPARGHA 406
 Db 339 -----HICFG----- 343
 QY 407 LLRWTLALLCLMVSAFSGFGPVTWLVSEIYPVEIRGAFACNSFNMAANLFISSLF 466
 Db 344 ---KYLAVTALTYIIAFFSATWGPVMWYIGESFPLKIRGLGVSFGAANVMAANWVVSILTF 401
 QY 467 LDIGITGLSWTFLLYGLTAVILGLGF 492
 Db 402 LPLLSFGTGKIFLIYACCFLSINP 427
 RESULT 14
 Q9LLE1 PRELIMINARY; PRT; 534 AA.
 AC Q9LLE1
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HEXOSE TRANSPORTER (FRAGMENT).
 GN PGCT.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20271774; PubMed=10810150;
 RA Weber A., Servaites J.C., Geiger D.R., Kofler H., Hille D., Groner F.,
 RA Hebbeker U., Flügge U.I.;
 RT "Identification, Purification, and Molecular Cloning of a Putative
 RT Plastidic Glucose Translocator.";
 RL Plant Cell 12:787-802(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
 DR EMBL; AF215852; AAF74566.1; .
 DR InterPro; IPR003662; sub.transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PRINTS; PR00171; SUGRTRNSPORT.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 534 AA; 56482 MW; 676A5E6C3C809ECA CRC64;

Query Match 18.8%; Score 519; DB 10; Length 534;
 Best Local Similarity 30.0%; Pred. No. 1.2e-22;
 Matches 158; Conservative 75; Mismatches 188; Indels 106; Gaps 12;

QY 4 SPVPLPLCASVSLGLTFGYELAVISGALLPLQIDFGL--SCLQDFLVGSLIGALLA 61

Db 90 SGSLVPI-VGVACLGALLFGYHLGVVNGALEYLAKDLGIVENTVTOGWIVSSVLACATVG 148
 QY 62 SLVGGFLIDCYGRKQAILGSLNVLGAGSLTGLAGSLAWLVLGRAVVGFAISLSSMACCI 121
 Db 149 SFTGGALADKFGRTKTFVLDLAIPAVGAPLCTTAQSVQAMIIIGRLLTGIGIGISSAIVPL 208
 QY 122 YVSELVGPQRQGVLSVLEAGITVIGILLSYALNYALAGTPMGRHMFQWATAPAVLQSL 181
 Db 209 YISEISPTIEIRGTGLTGNOLFICIGILVALVAGLPLSGNPLMWRMTMFGIALIPSVLLAIG 268
 QY 182 LLFLPAG-----TDETATH-----KDLIPLQGG--EAPKLGPRYSFLDLFRA 224
 Db 269 MAFSPESPRWLFQOGRISAEISIRKLYKERVAVGVGDLEASAQSSSEPDAGNLDLFS 328
 QY 225 RDNMRGRTTVGLGLVLFQOLTGPQNVLYCYASTIFSSVCFHGGSSAVLASVCLGAVKVAAT 284
 Db 329 R-YMKVVSIGAAFLFOOFAGINAVVYSTAVERSAGI---SSDVAASALYCAANVFCT 383
 QY 285 LTAMGLVDRAGRALLAGCALMALSVSGILVSFAVPMDSGSPCLAVPNATGOTGLPGD 344
 Db 384 MVASSLMDKQGRKSL-----LVSF-----TCMAAS 409
 QY 345 SGLLDSSLPPIPTNEDQREPILSTAKTKPHPRSGDPSAPPRLALSSALPGPPLPARG 404
 Db 410 NMLLS-----LSFTWKVLT-PYSGT----- 428
 QY 405 HALLRWTLALLCLMVSAFSGFGPVTWLVSEIYPVEIRGAFACNSFNMAANLFISSL 464
 Db 429 -----LAVLCTVLYVLSFSLGAGVPVALLPEIFASIRAKAVALSGLCHMHWISNFFIGL 482
 QY 465 SFLDLIGITGLSWTFLLYGLTAVILGLGFYFVPEPKGOSLAIDQO 511
 Db 483 YFLSIVTKEGISTVYLGFAVCCLLAVNVIYGVNVTGKRSLEDIERE 529
 RESULT 15
 Q9LLE0 PRELIMINARY; PRT; 470 AA.
 AC Q9LLE0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HEXOSE TRANSPORTER (FRAGMENT).
 GN PGCT.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20271774; PubMed=10810150;
 RA Weber A., Servaites J.C., Geiger D.R., Kofler H., Hille D., Groner F.,
 RA Hebbeker U., Flügge U.I.;
 RT "Identification, Purification, and Molecular Cloning of a Putative
 RT Plastidic Glucose Translocator.";
 RL Plant Cell 12:787-802(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
 DR EMBL; AF215853; AAF74567.1; .
 DR InterPro; IPR003662; sub.transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PRINTS; PR00171; SUGRTRNSPORT.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 470 AA; 49667 MW; FC11D804C93ED71 CRC64;

Query Match 18.7%; Score 516; DB 10; Length 470;
 Best Local Similarity 28.8%; Pred. No. 1.5e-22;

Matches 152; Conservative 83; Mismatches 186; Indels 106; Gaps 11;

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QY 4 SPVPLPCASVSLGLTGGVLAIVSGALLPLQLDFCL--SCLEQEFVYVCSLLGLGALLA 61
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 26 SGVLPY-VGVACLGAILFGYHLCVNGALEYLAKEGTAENTVIOGWIVSTVLGAFVG 84
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 62 SLVGGFLIDCYGRKQATLGSNLVLLAGSLTGLAGSLANIWLGRVAVVGFATSLSSMACCI 121
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 85 SFTGGVLADRFGRKTKFILDAPLSVCAFLCTTAQSVQAMIIIGRLTGTIGIGISSAIVPL 144
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 122 YVSELVGPORGVLSVLYEAGITVIGILLSYALNYALAGTPWGRHMFGNATAPAVLOSLS 181
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 145 YISEISPTFIRGTGLTVNQNFICIGILVALVGLPLSGNPSMWRMTFGLALIPSVLLAIG 204
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 182 LLELPAG-----TDETAT-----HKDLIPLOGG-EAPKLGGRPRYSFLDLFRA 224
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 205 MAFSPESPRLYQOGRISEAETSIRKLYGKEKVAEYVWGDLEASARGSSRPDAGWLDLFSS 264
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 225 RDNHGRGTTVGLGLVLFQQLTGQPNVLCYASTIFSSVGHGSSAVLASVGLGAVKVAAT 284
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 265 R--YRKVVSIGAAHFLQQLAGINAVVYSTAVFRSAGI---TSDVAASALVGAANVFGT 319
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 285 LTAMGLVDRAGREALLACALMALSVSGIGLVSPFVPMWDSGPSCLAVPNATGOTGLPGD 344
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 320 TVASSLMDKQGRKSLLSISYTGMAASMLLSL-SF----- 353
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 345 SGLLDSSLPPIPTNEDQREPISTAKTKPHPRSGDPSPAPRLALSSALPGPPLPARG 404
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 354 -----TWKVLTPY--SGT----- 364
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 405 HALLRTALLCLMVFYSAFSGFGPVTWLVLSIYVEIRGRAPAFCSFNNAANLFI 464
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 365 -----LAVLGTVLYVLSFSLGAGPVALLPEIFASIRAKAVALSGLGVHWMNPF 418
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
QY 465 SFLLDGLTIGLSWTFLLYGLTAVLGLGYFLFVPETKGOSLAEDQO 511
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |
Db 419 YFLSVTKFGISTVYMGFALSCLVAVVYITGNVVKGRSLEEIERE 465
| | | | | : | | : | | | | | | | | | | | : | | : | | | | |

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Search completed: March 15, 2002, 07:09:18
Job time: 329 sec